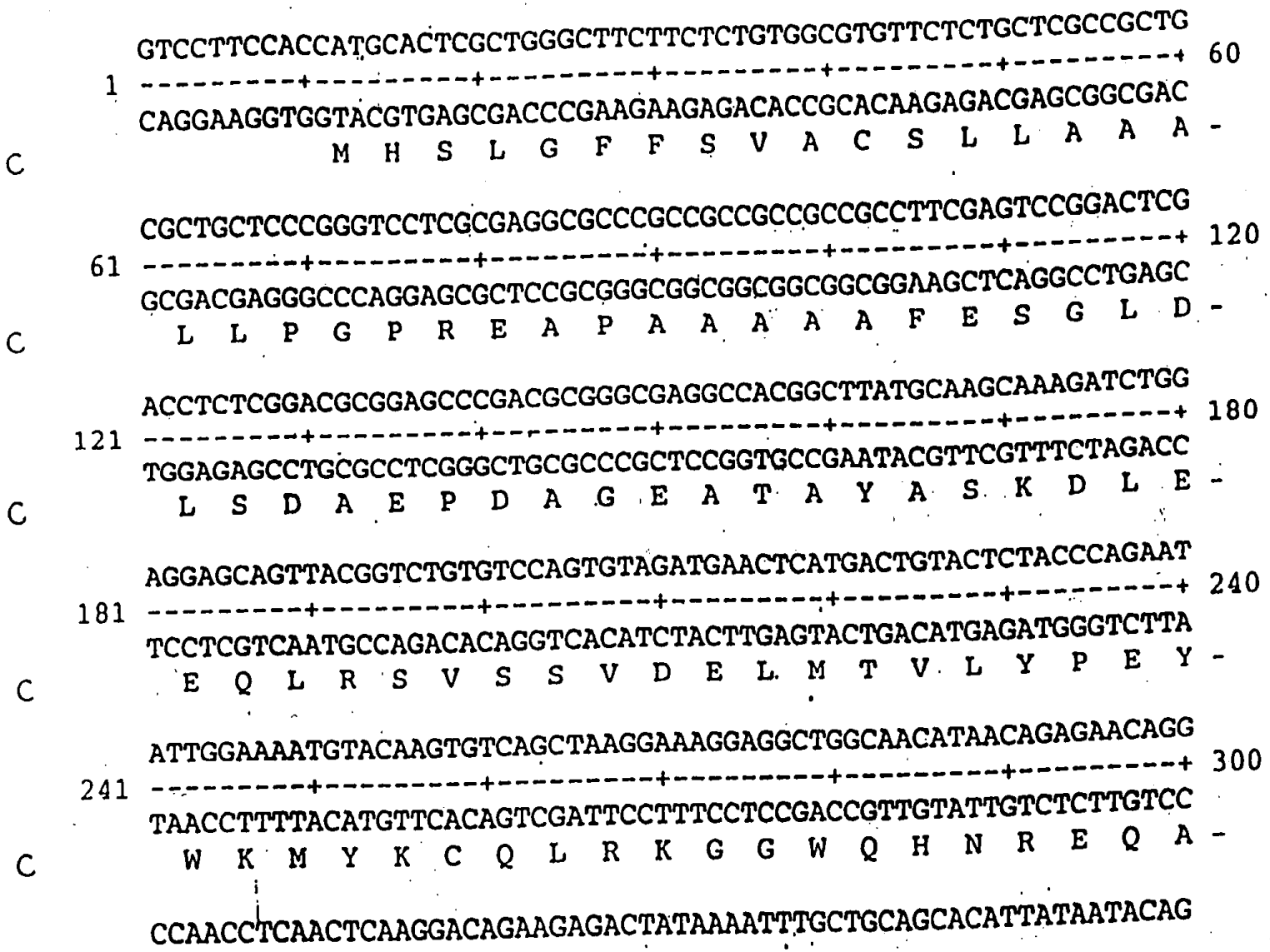
FIG. 1A



MATCH WITH FIG. 1B

FIG. 1B

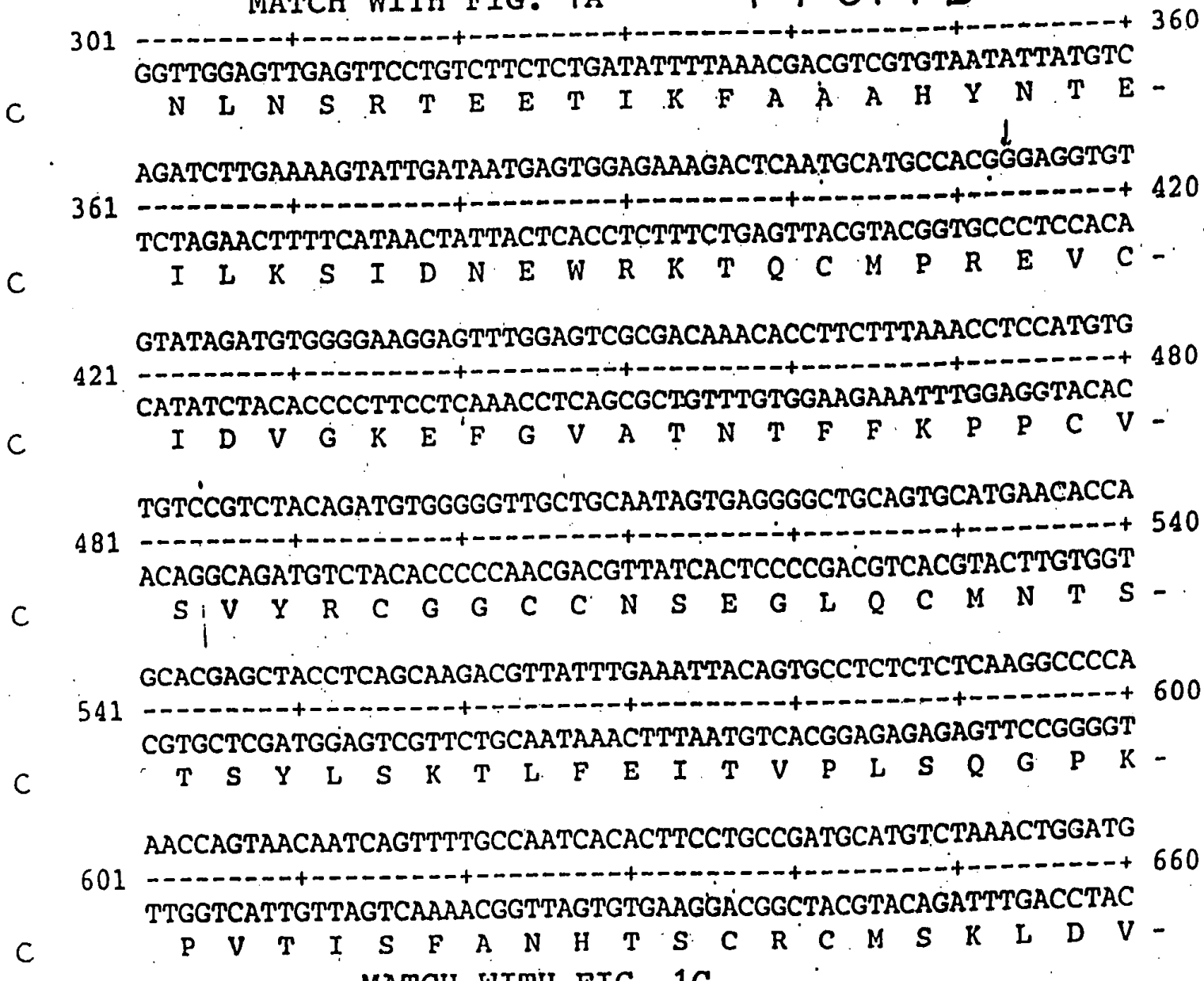
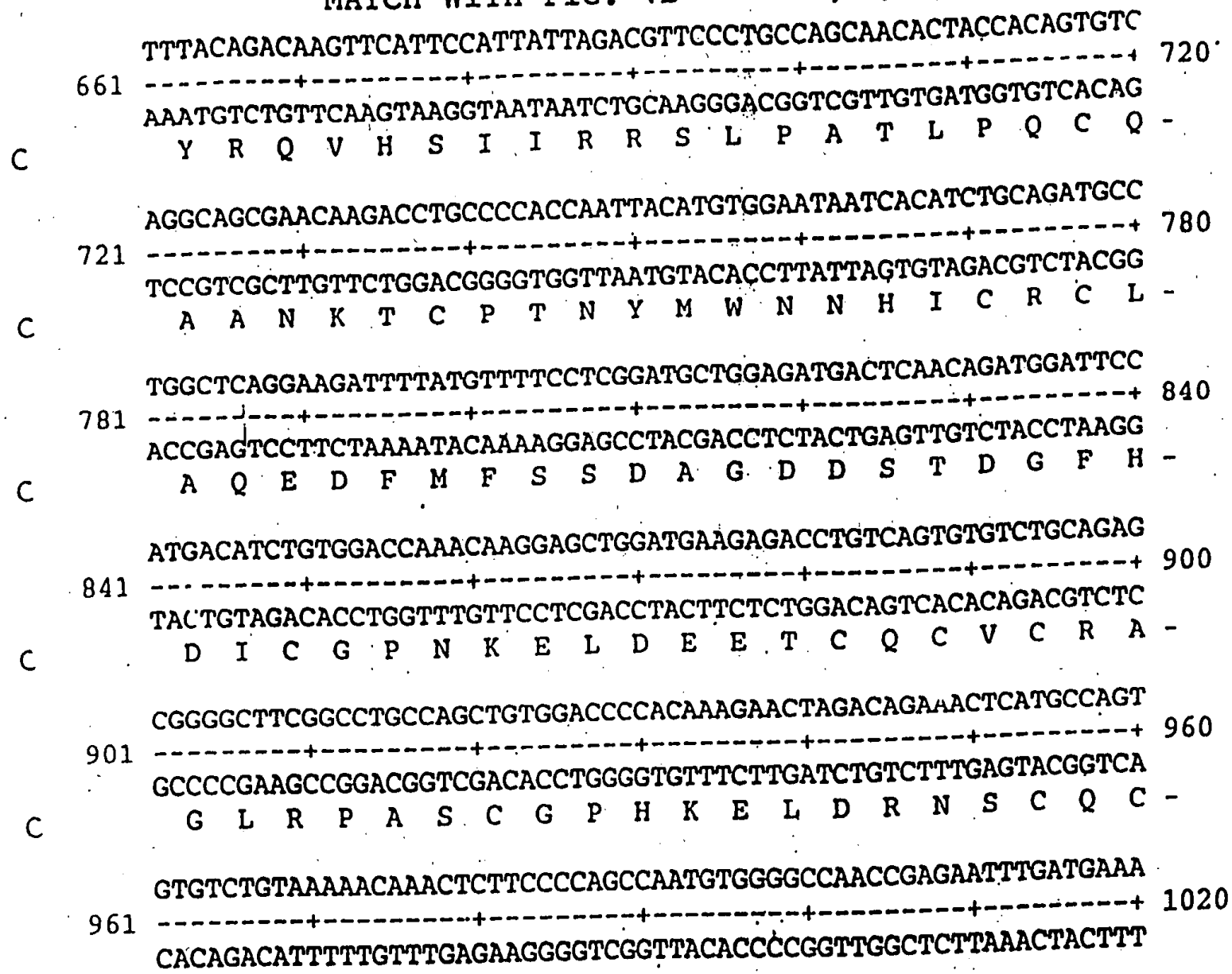

MATCH WITH FIG. 1A
301
360
GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
C N L N S R T E E T I K F A A A H Y N T E -
AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361
420
TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
C I L K S I D N E W R K T Q C M P R E V C -
GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
421
480
CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
C I D V G K E F G V A T N T F F K P P C V -
TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481
540
ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
C S V Y R C G G C C N S E G L Q C M N T S -
GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
541
600
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
C T S Y L S K T L F E I T V P L S Q G P K -
AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601
660
TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
C P V T I S F A N H T S C R C M S K L D V -
MATCH WITH FIG. 1C

FIG. 1C

MATCH WITH FIG. 1B



MATCH WITH FIG. 1D

FIG. 1D

MATCH WITH FIG. 1C

```
C        V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

         ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021     ---------+---------+---------+---------+---------+---------+---------+ 1080
         TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
C          T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

         AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081     ---------+---------+---------+---------+---------+---------+---------+ 1140
         TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
C          C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

         ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141     ---------+---------+---------+---------+---------+---------+---------+ 1200
         TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
C          H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

         CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201     ---------+---------+---------+---------+---------+---------+---------+ 1260
         GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
C          G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

         AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

FIG. 1E

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
C      M  S  *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 -- ------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

```
  1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
     ---------+---------+---------+---------+---------+---------+---------+

 71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
     ---------+---------+---------+---------+---------+---------+---------+
              M   T   V   L   Y   P   E   Y   W   K   M   Y   K   C   Q   L   R

121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
     ---------+---------+---------+---------+---------+---------+---------+
      K   G   G   W   Q   H   N   R   E   Q   A   N   L   N   S   R   T   E   E   T

181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
     ---------+---------+---------+---------+---------+---------+---------+
      I   K   F   A   A   A   H   Y   N   T   E   I   L   K   S   I   D   N   E   W

241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
     ---------+---------+---------+---------+---------+---------+---------+
      R   K   T   Q   C   M   P   R   E   V   C   I   D   V   G   K   E   F   G   V

301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
     ---------+---------+---------+---------+---------+---------+---------+
      A   T   N   T   F   F   K   P   P   C   V   S   V   Y   R   C   G   G   C   C
```

FIG. 2A

```
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     --------+---------+---------+---------+---------+---------+---------+
      N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     --------+---------+---------+---------+---------+---------+---------+
      E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     --------+---------+---------+---------+---------+---------+---------+
      T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     --------+---------+---------+---------+---------+---------+---------+
      R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     --------+---------+---------+---------+---------+---------+---------+
      Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     --------+---------+---------+---------+---------+---------+---------+
      D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG.2B

```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ---------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ---------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ---------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ---------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ---------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ---------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

```
1081  TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCA
      ---------+---------+---------+---------+---------+---------+
       R  C  V  P  S  Y  W  Q  R  P  Q  M  S

1141  GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
      ---------+---------+---------+---------+---------+---------+

1201  GAGACCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCTGAACCATGTGGA
      ---------+---------+---------+---------+---------+---------+

1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTT
      ---------+---------+---------+---------+---------+---------+

1321  CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA
      ---------+---------+---------+---------+---------+---------+

1381  TAATTTATTTCCACTAAAAATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGT
      ---------+---------+---------+---------+---------+---------+

1441  AAAACTCACTGTGATCAATATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAA
      ---------+---------+---------+---------+---------+---------+

1501  TTGTATTATAAAAAAAAAAAAAAA
      --------+---------+------
```

FIG. 2D

```
        1                                                   50
Pdgfa   .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb   MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf   .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2   .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

        51                                                 100
Pdgfa   IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb   GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf   APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2   REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

        101                                                150
Pdgfa   AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb   AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf   SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2   TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

        151                                                200
Pdgfa   RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb   QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf   EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2   STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

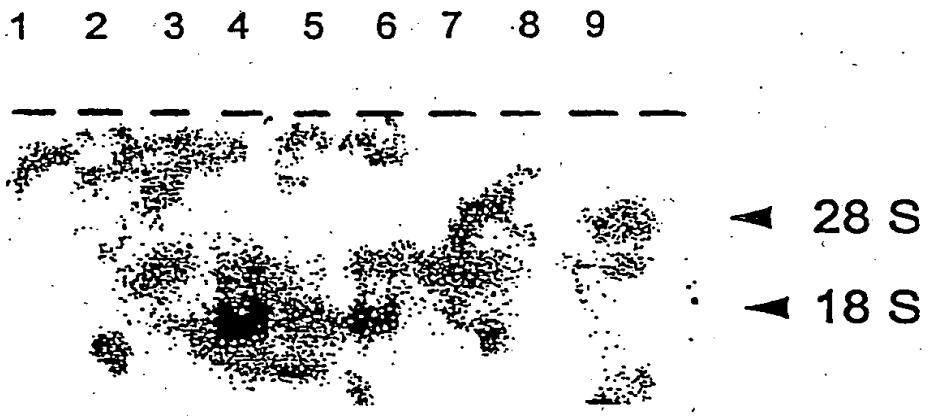
```
        201                                                        250
Pdgfa   ....TSLNPD YREEDTDVR. .......... .......... ..........
Pdgfb   RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf   RGK........ .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2   RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

        251                                                        300
Pdgfa   .......... .......... .......... .......... ..........
Pdgfb   A......... .......... .......... .......... ..........
 Vegf   ....CGP.... .......... .......CSE RRKHLFVQDP QTCKCSCKNT
Vegf2   FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

        301                                                        350
Pdgfa   .......... .......... .......... .......... ..........
Pdgfb   .......... .......... .......... .......... ..........
 Vegf   ..DSRCKARQ LELNERTCRC DKPRR..... .......... ..........
Vegf2   LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

        351                                                    398
Pdgfa   .......... .......... .......... .......... ........
Pdgfb   .......... .......... .......... .......... ........
 Vegf   .......... .......... .......... .......... ........
Vegf2   KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE				
	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

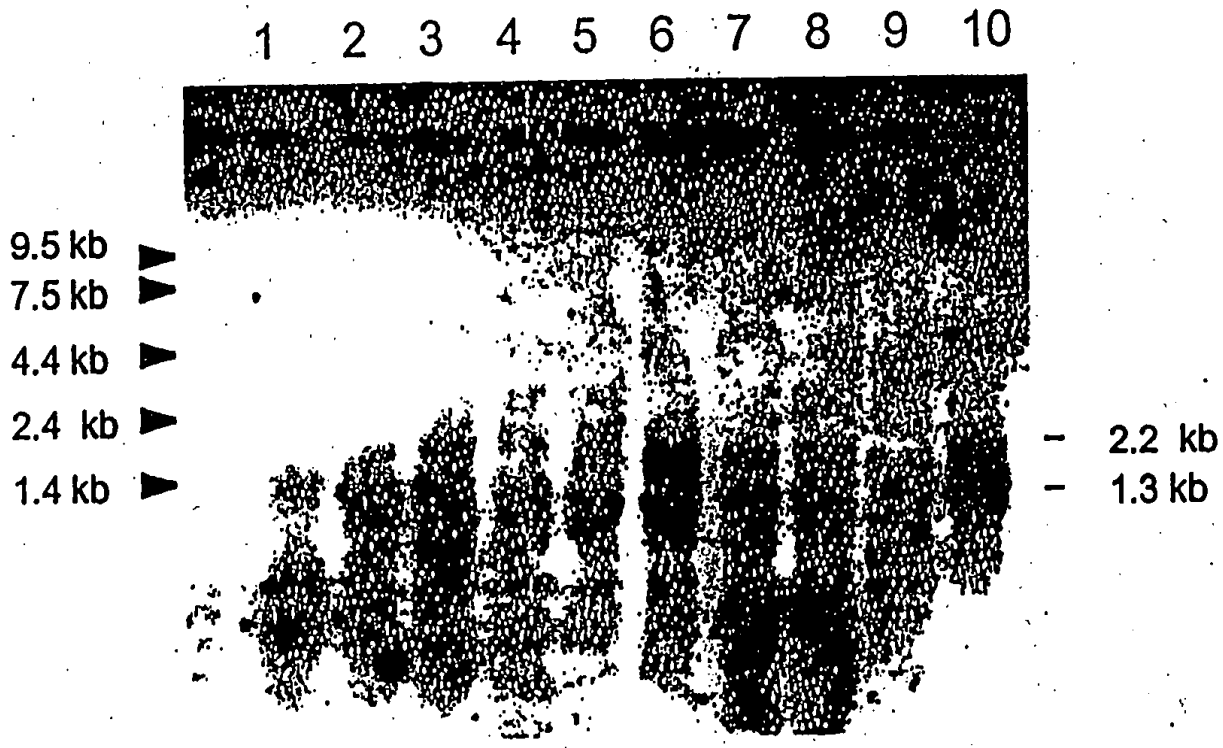
FIG. 4

Expression of VEGF2 mRNA in
Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
3-9. breast tumor cell lines.

FIG. 5

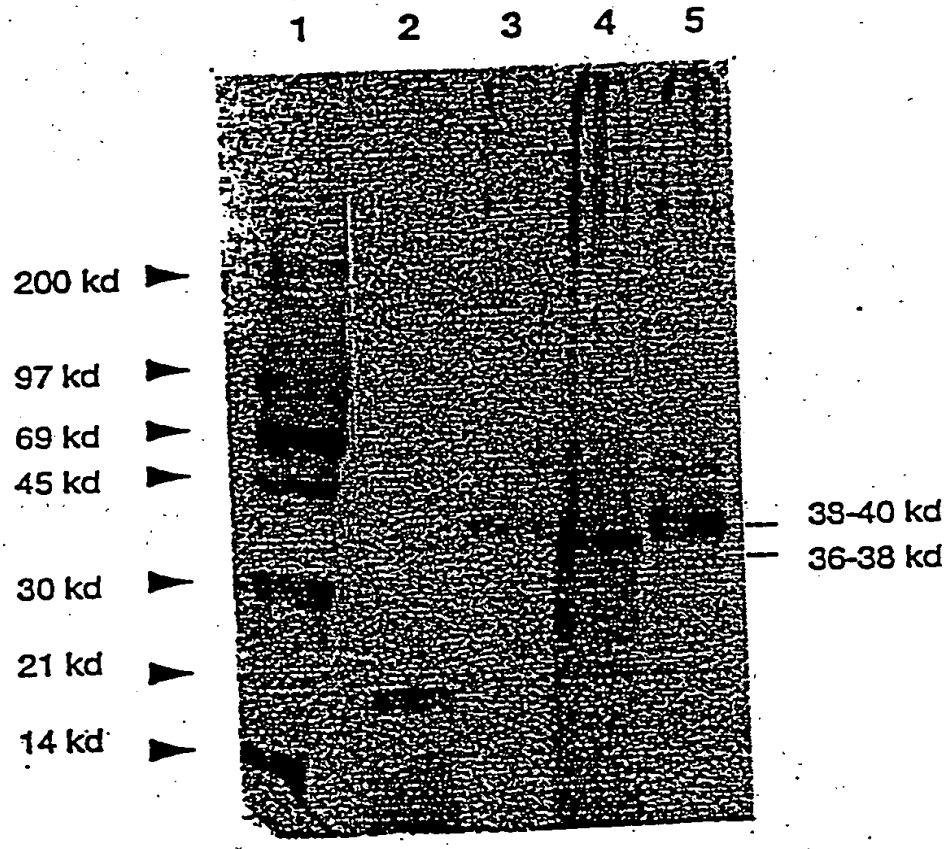


1.	ovary	6.	lung
2.	testes	7.	spleen
3.	gall bladder	8.	prostate
4.	kidney	9.	Hippocampus
5.	liver	10.	heart

Expression of VEGF2 mRNA in human adult tissues.

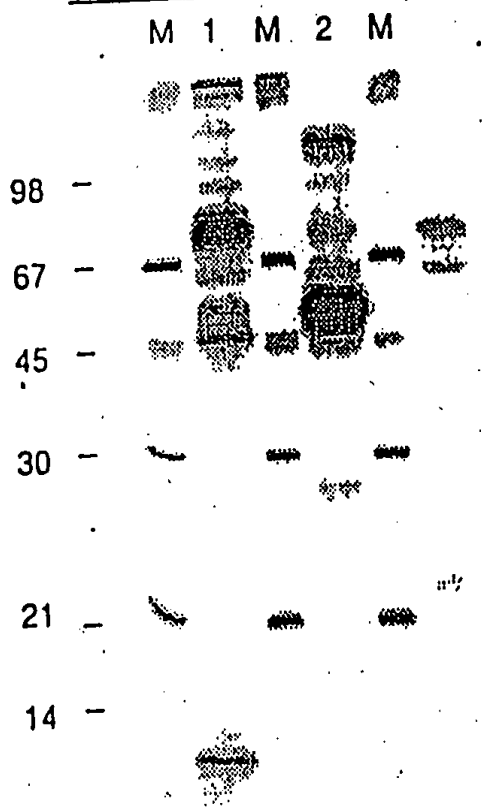
FIG. 6

FIG. 7



Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse & forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

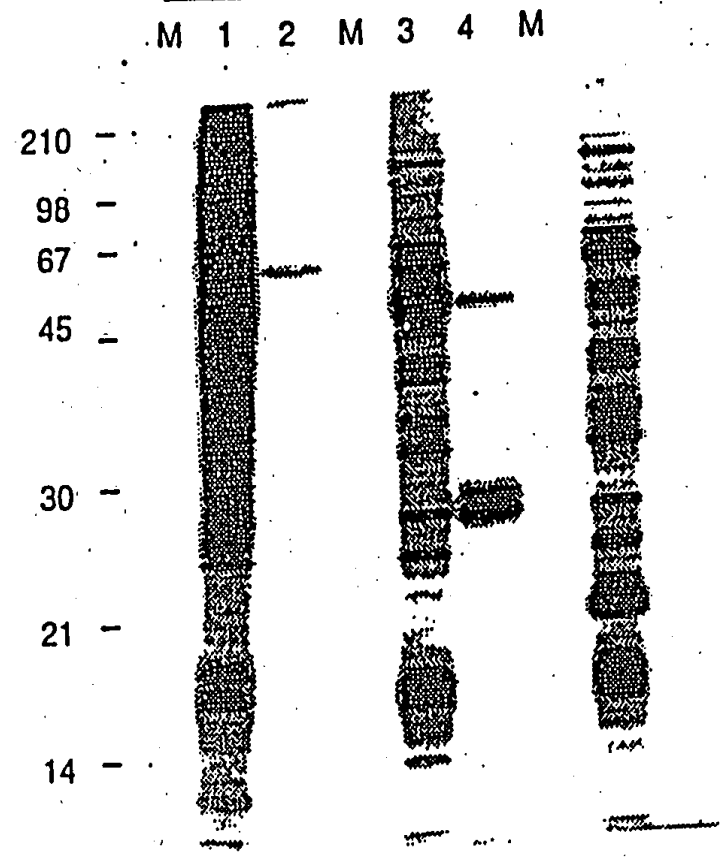
non-reducing gel



Lane M: Marker
Lane 1: vector medium
Lane 2: VEGF2 medium

FIG. 8A

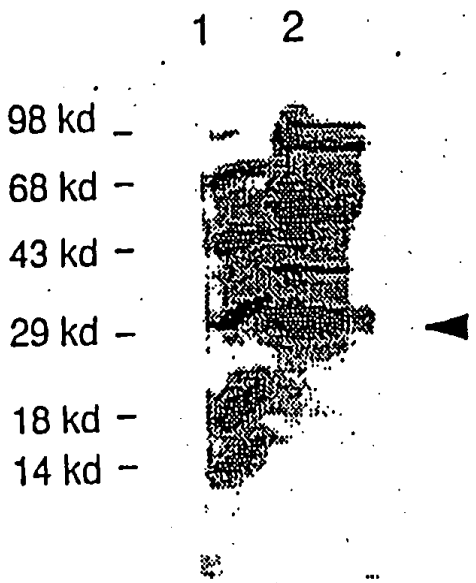
reducing gel



Lane M: Marker
Lane 1: vector cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 cytoplasm
Lane 4: VEGF2 medium

FIG. 8B

FIG. 9



Lane 1: Molelular weight marker
Lane 2. Precipitates containing VEGF2.

FIG. 10

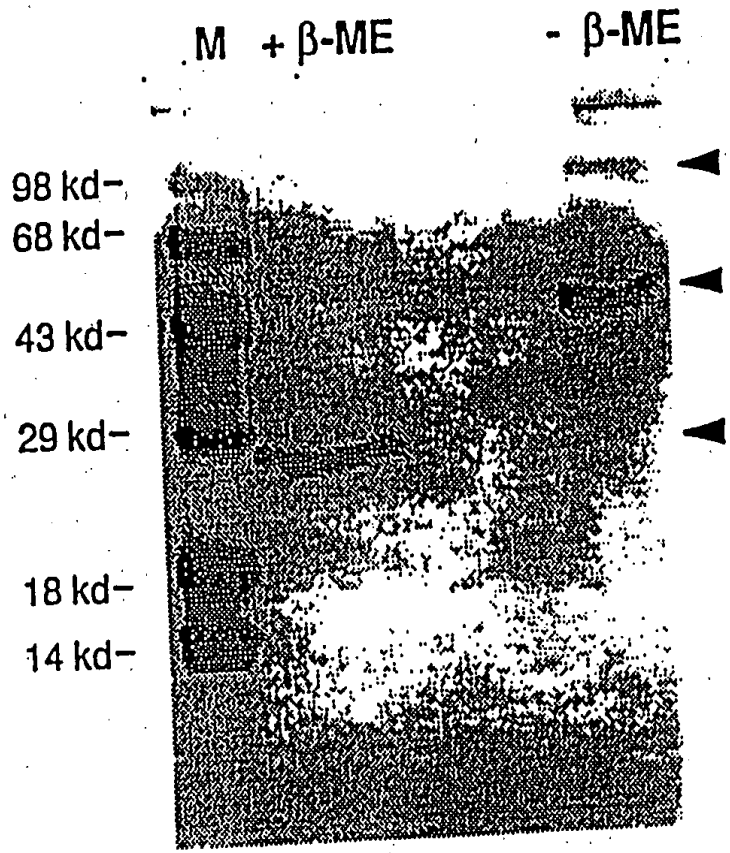


FIG. 11

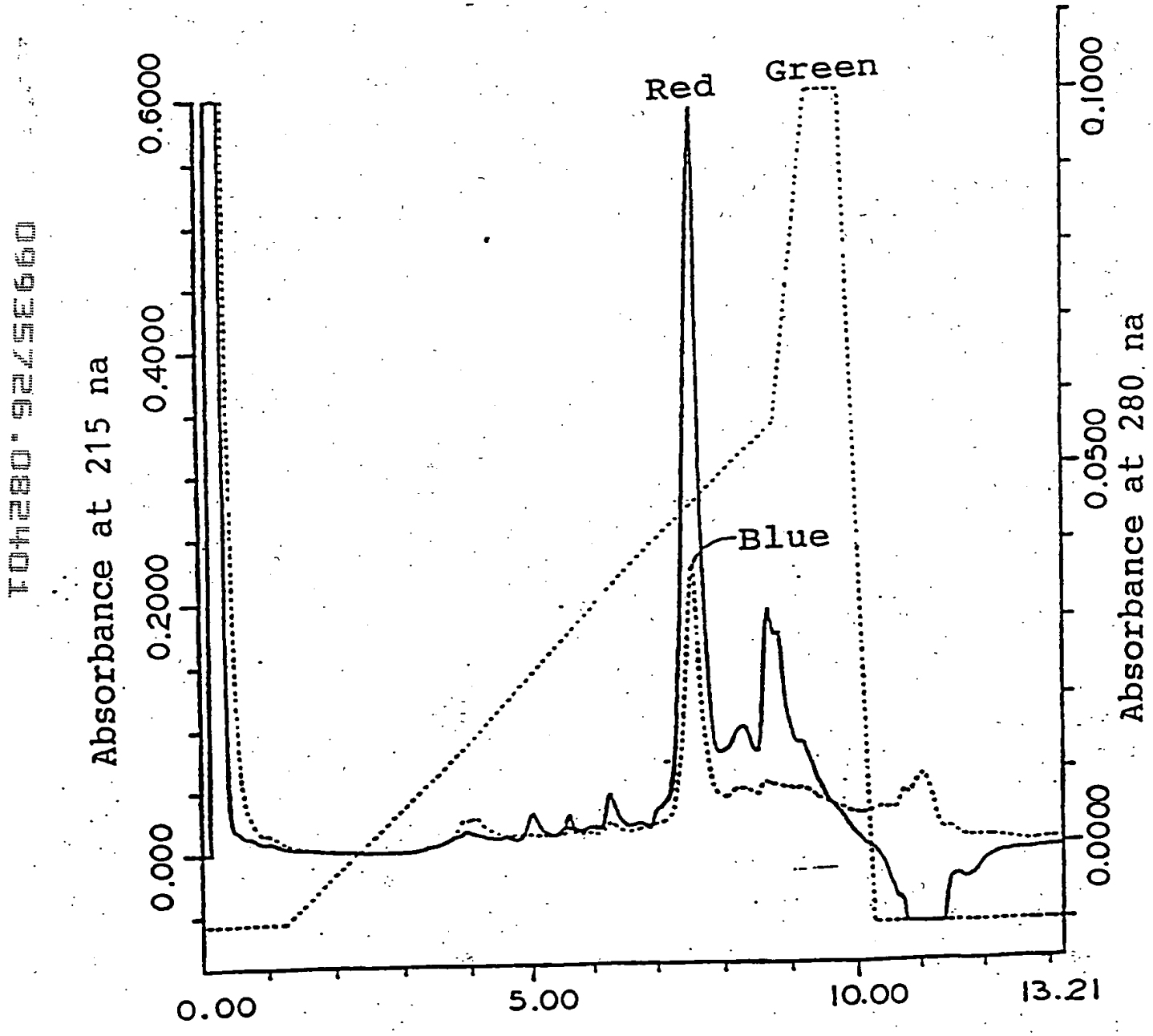

Red
Green
Blue
Absorbance at 215 na
Absorbance at 280 na
0.6000
0.4000
0.2000
0.000
0.1000
0.0500
0.0000
0.00
5.00
10.00
13.21

FIG. 12

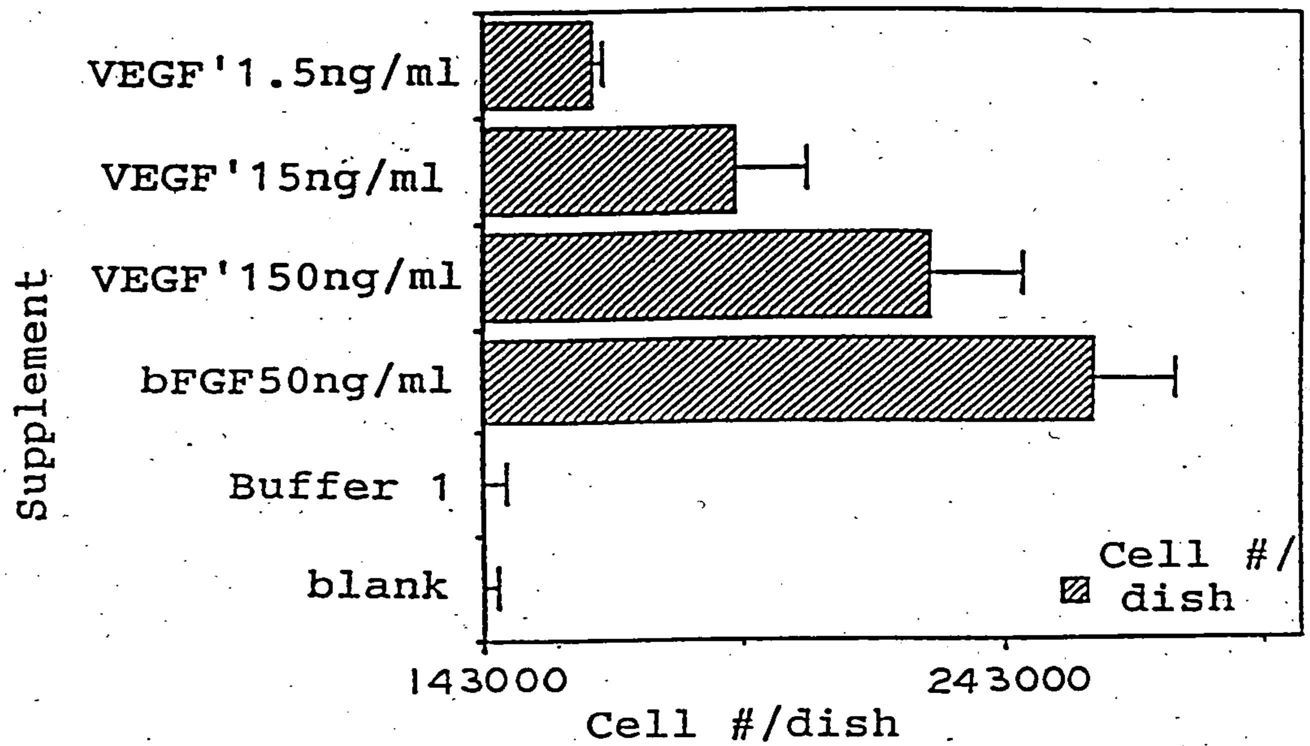
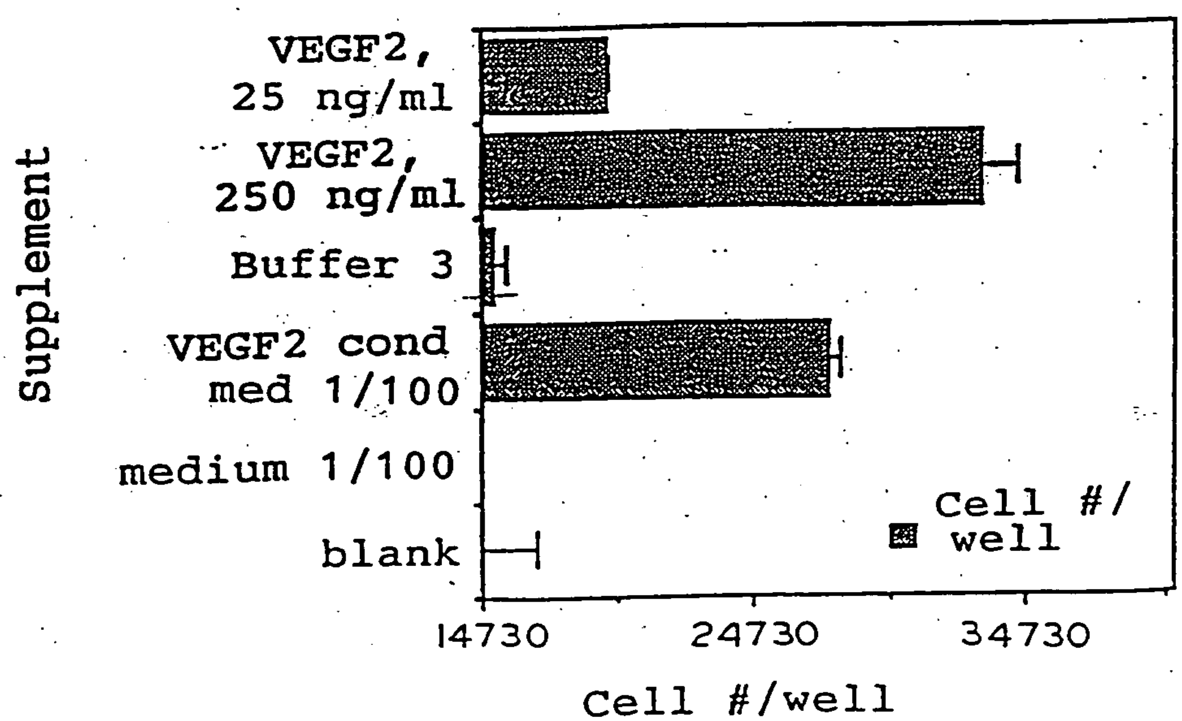

VEGF'1.5ng/ml
VEGF'15ng/ml
VEGF'150ng/ml
bFGF50ng/ml
Buffer 1
blank
Supplement
Cell #/ dish
143000
243000
Cell #/dish

FIG. 13


VEGF2, 25 ng/ml
VEGF2, 250 ng/ml
Buffer 3
VEGF2 cond med 1/100
medium 1/100
blank
Supplement
Cell #/ well
14730
24730
34730
Cell #/well

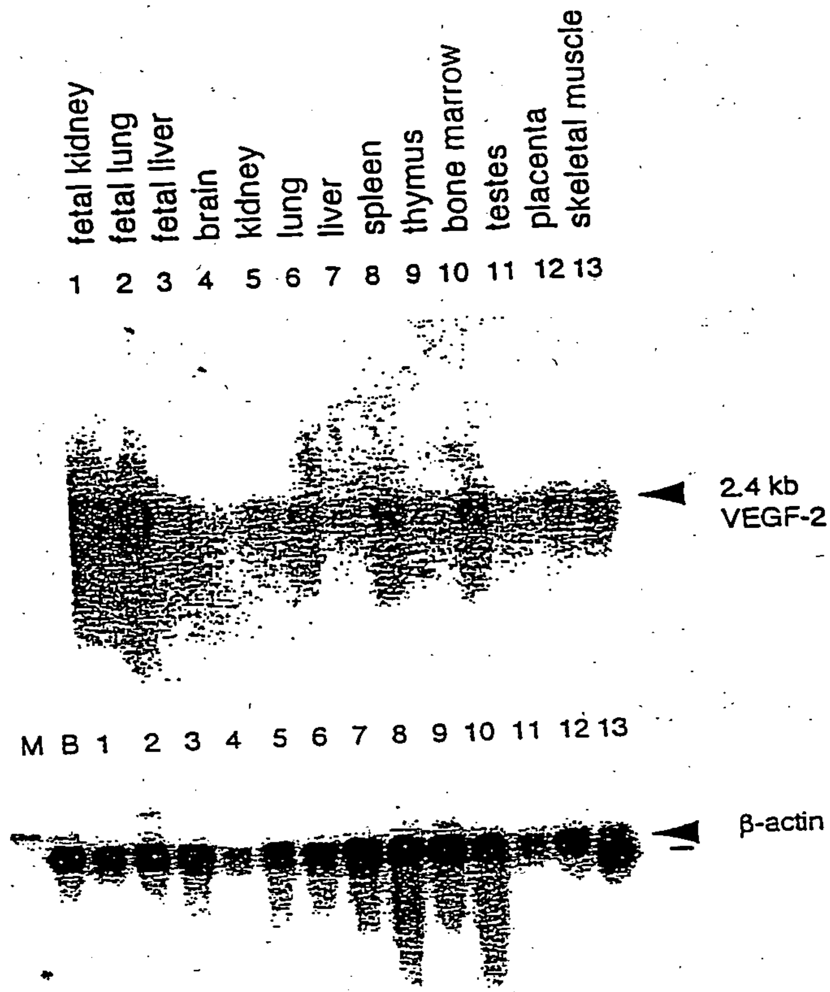
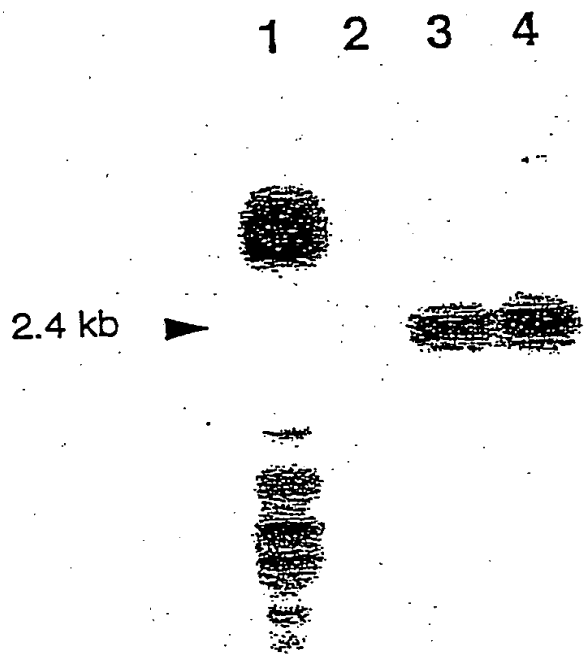


Figure 14



1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

Figure 15

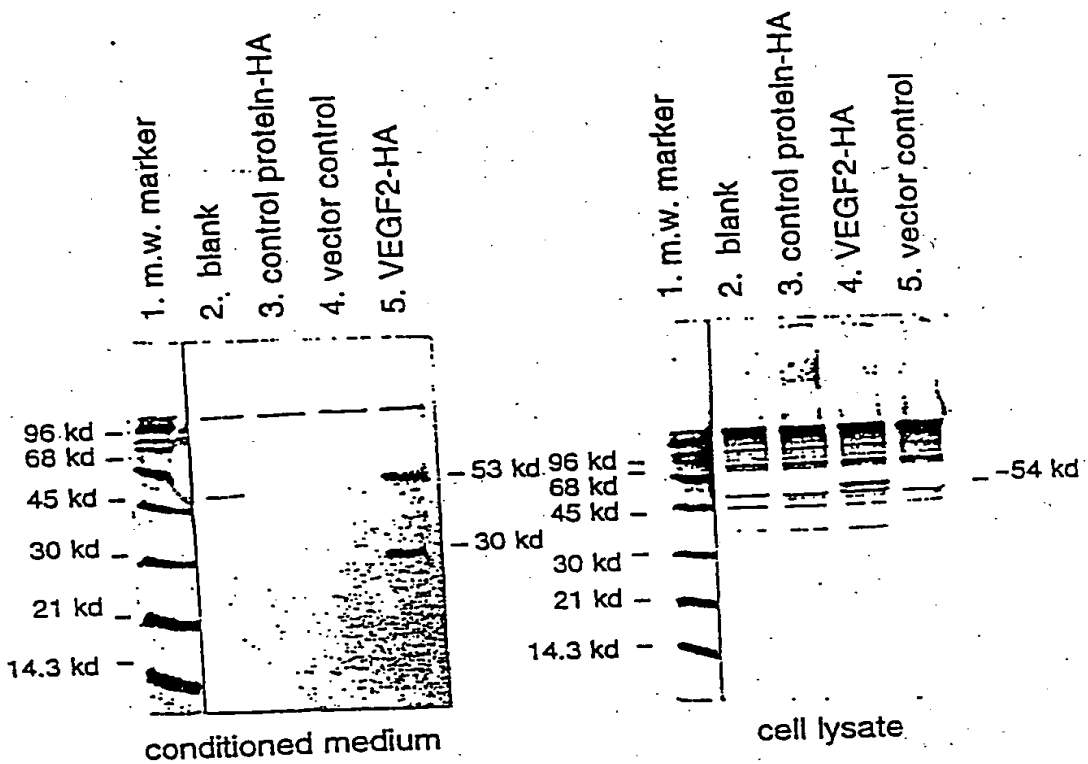


Figure 16

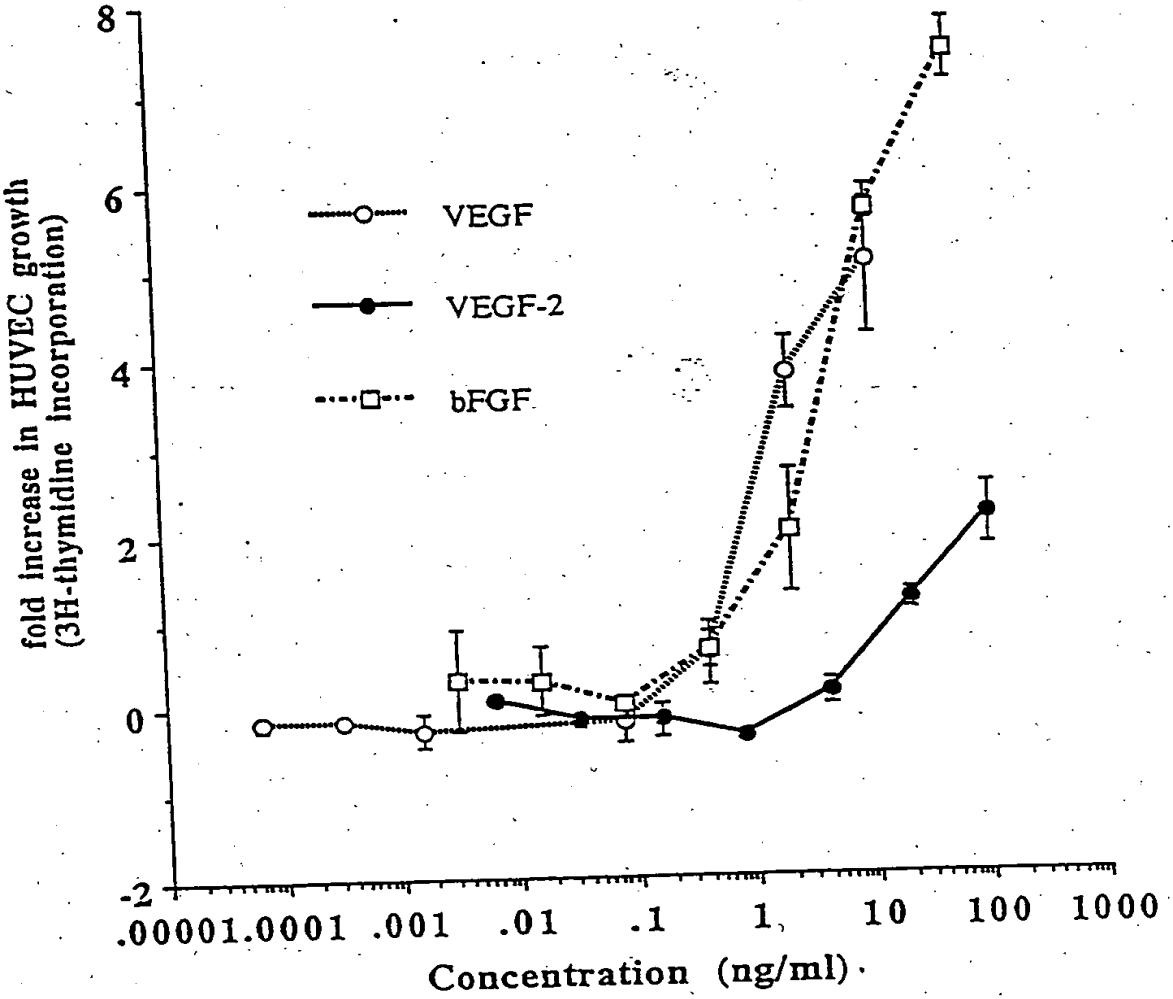


Figure 17

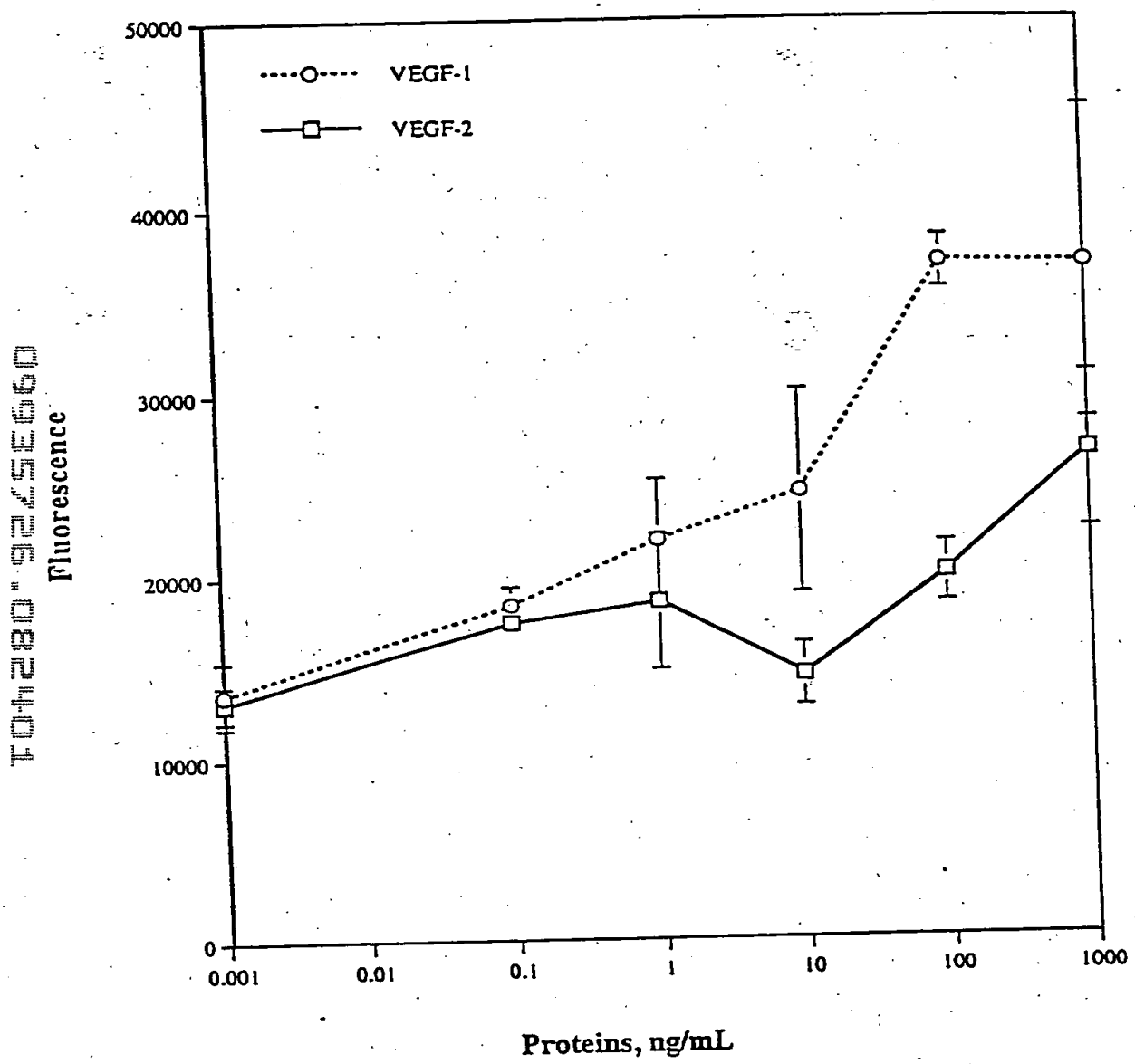

VEGF-1
VEGF-2
50000
40000
30000
20000
10000
0
0.001
0.01
0.1
1
10
100
1000
Fluorescence
Proteins, ng/mL

Figure 18

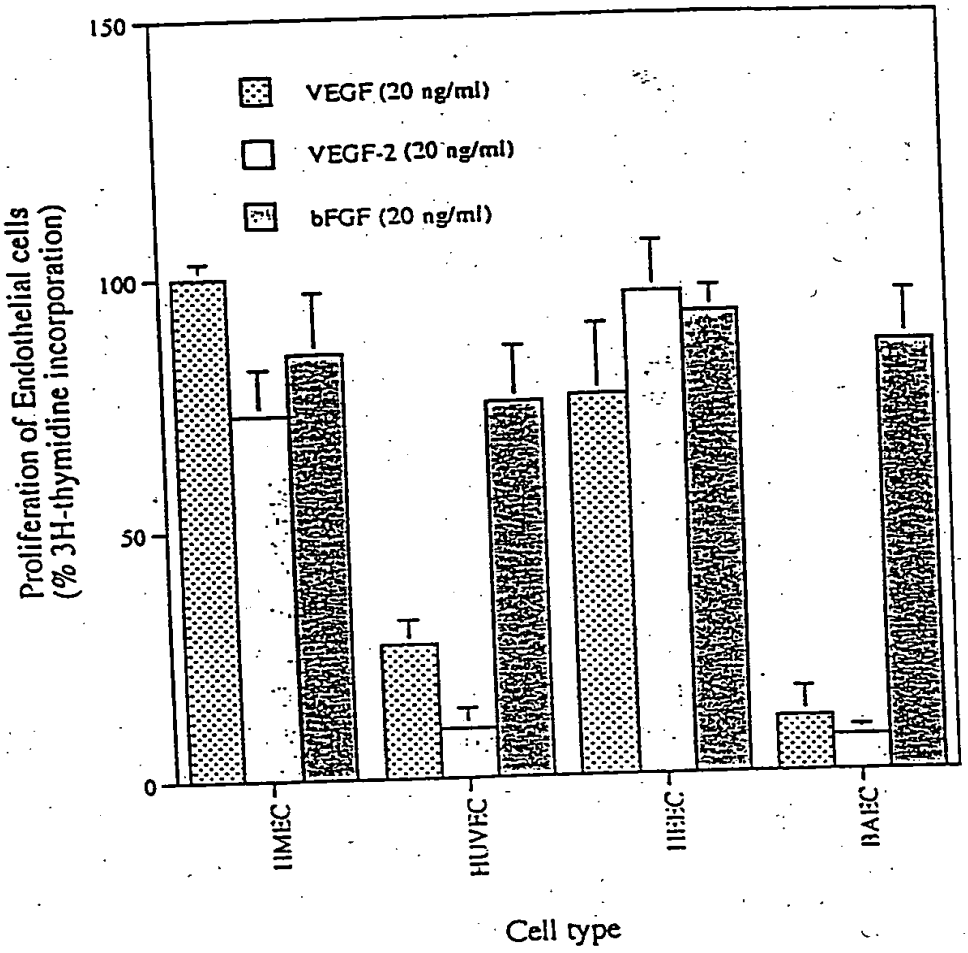


Figure 19

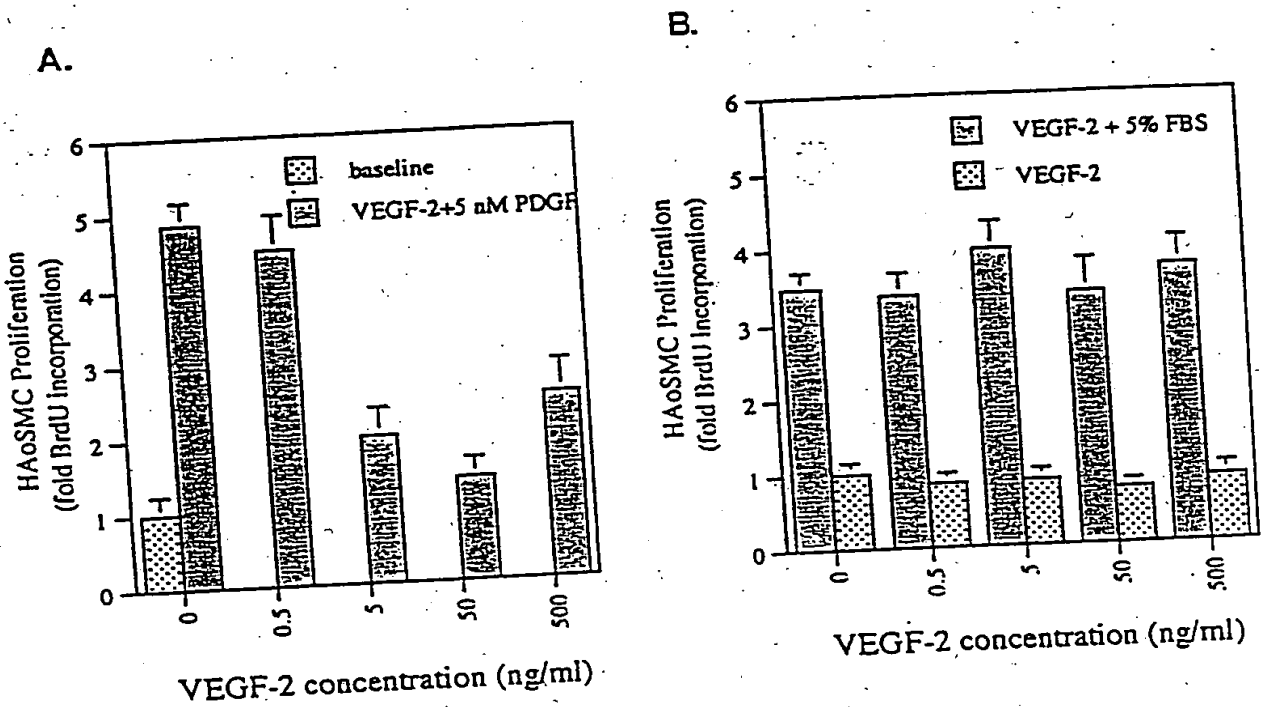
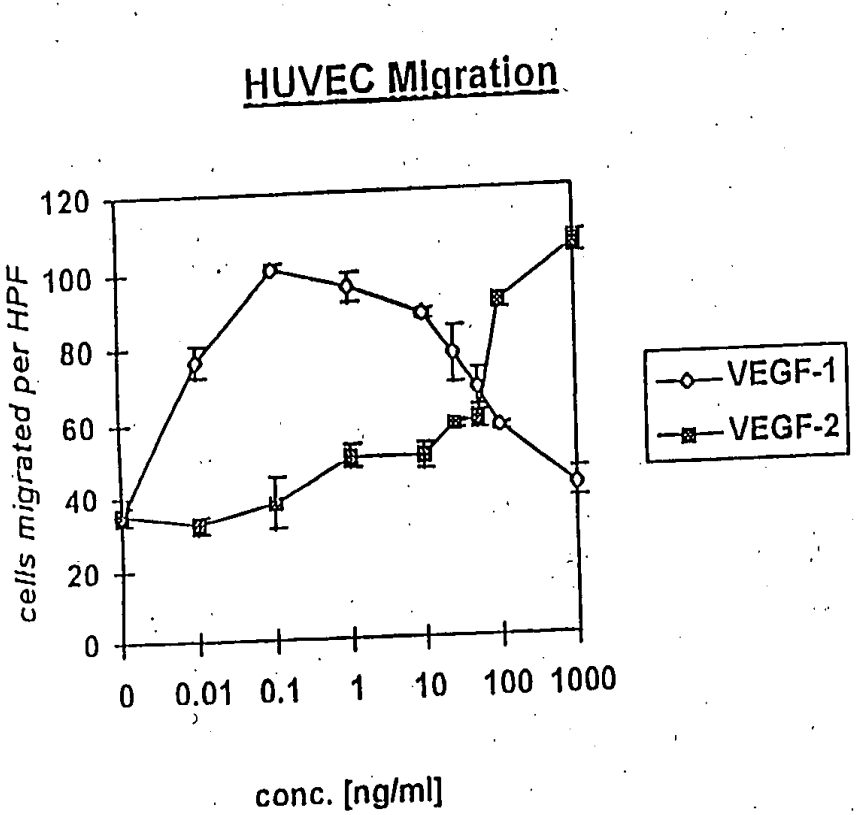


Figure 20



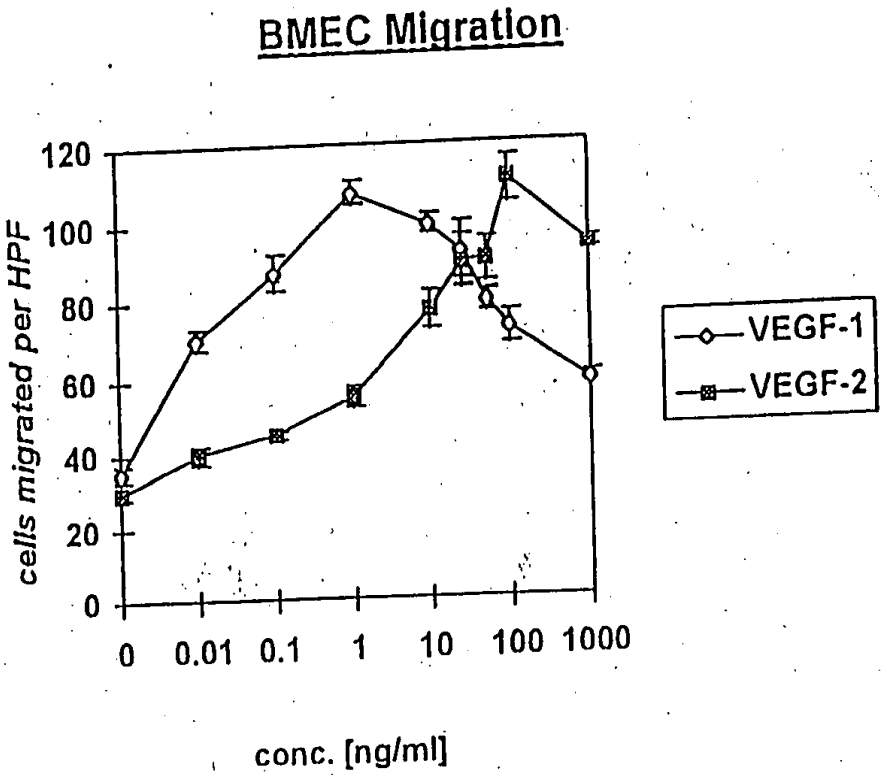


Figure 21

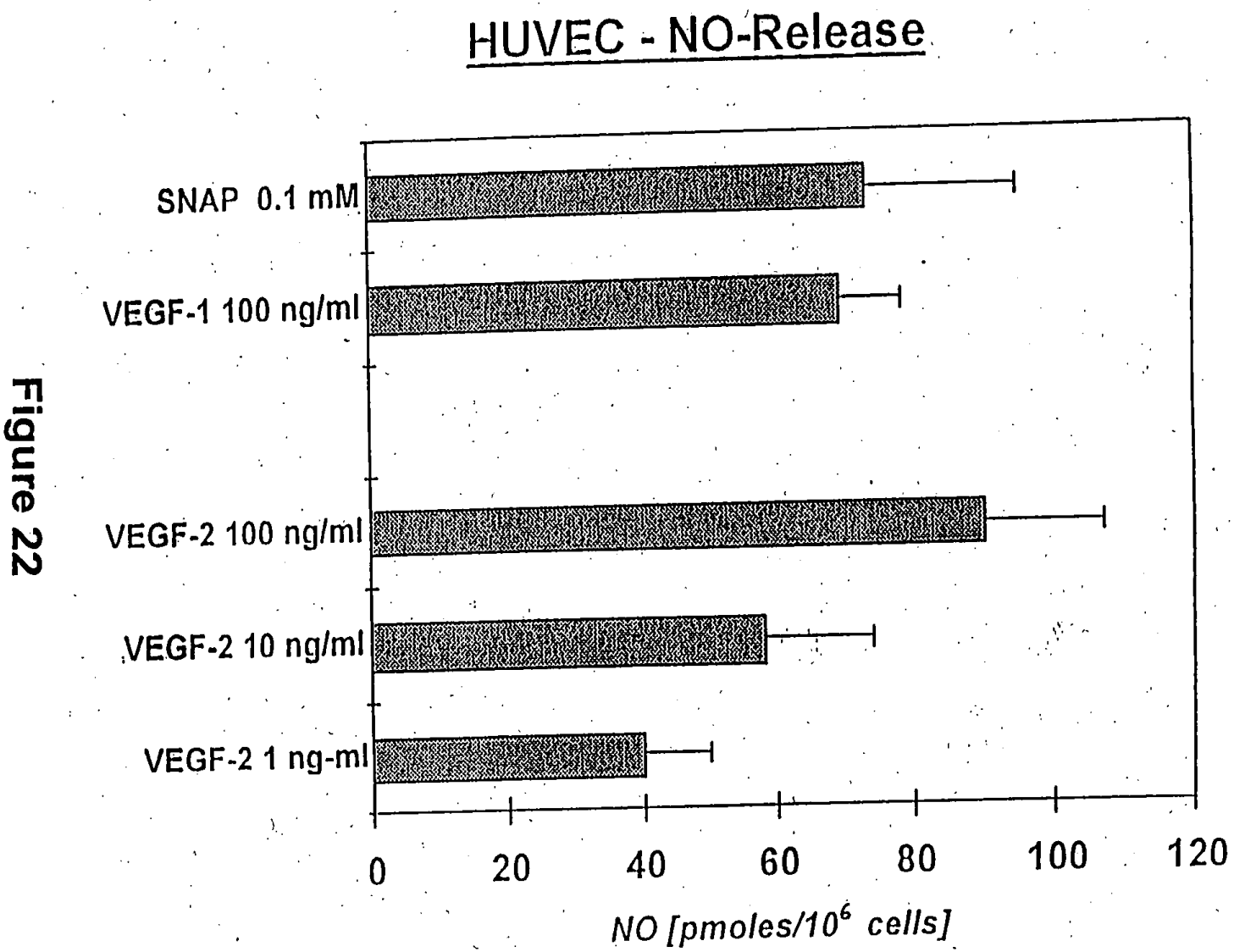


Figure 22

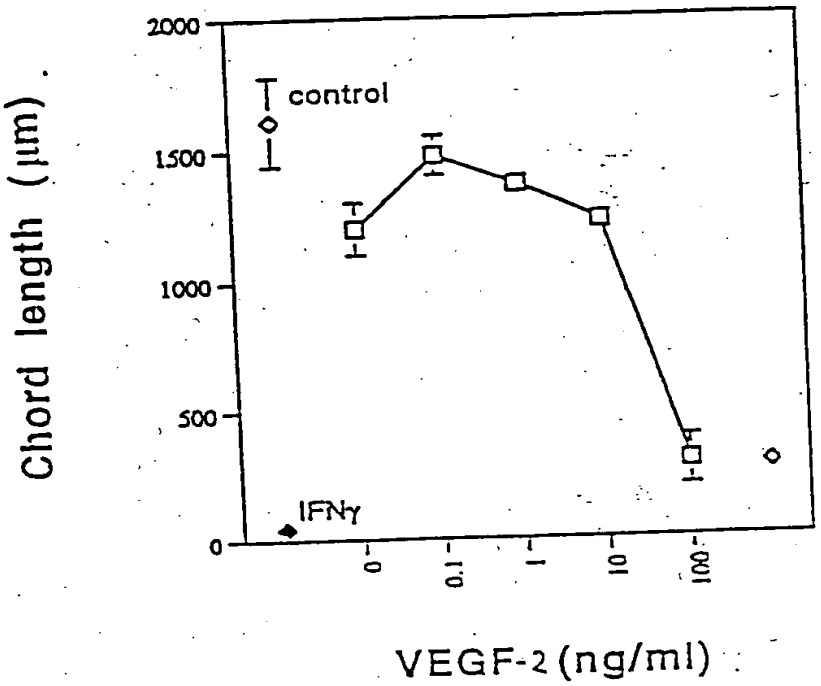


Figure 23

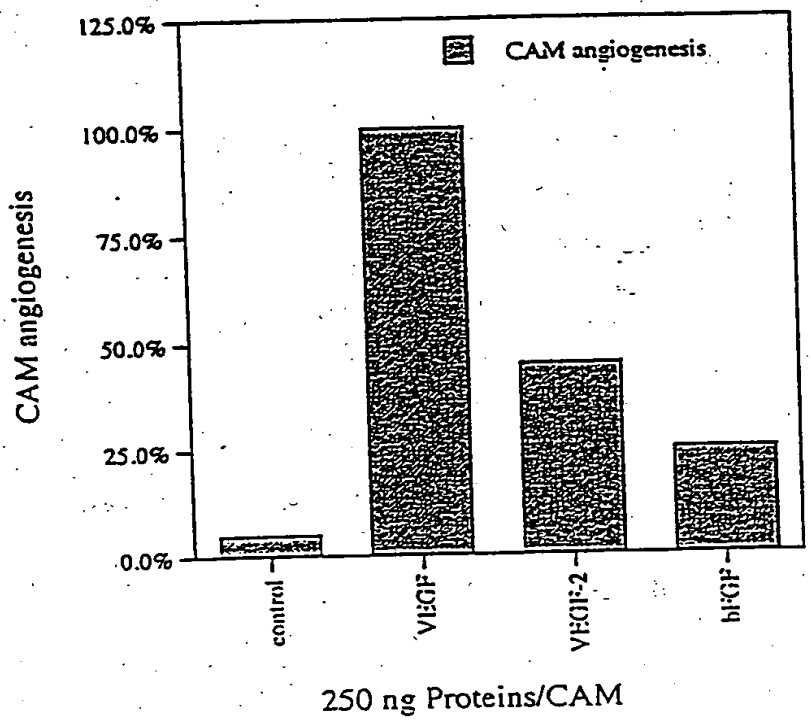
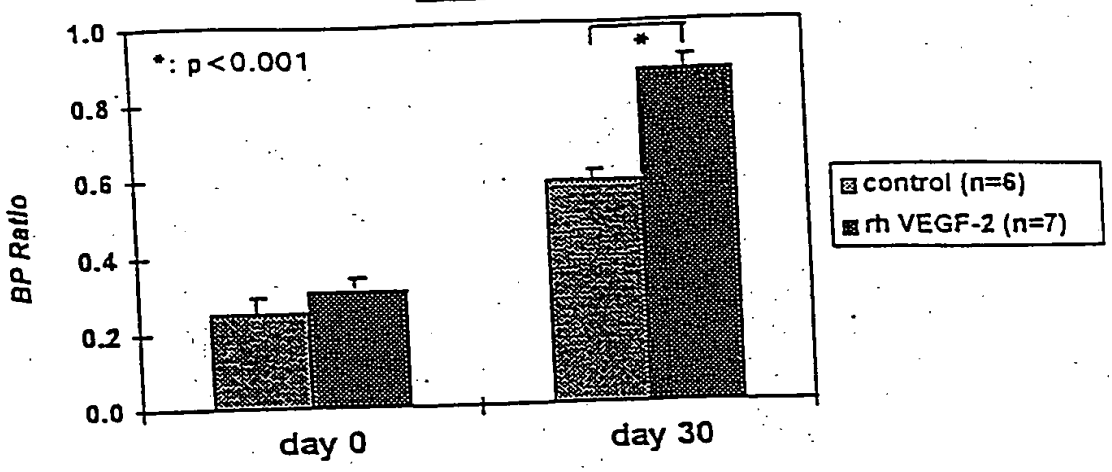
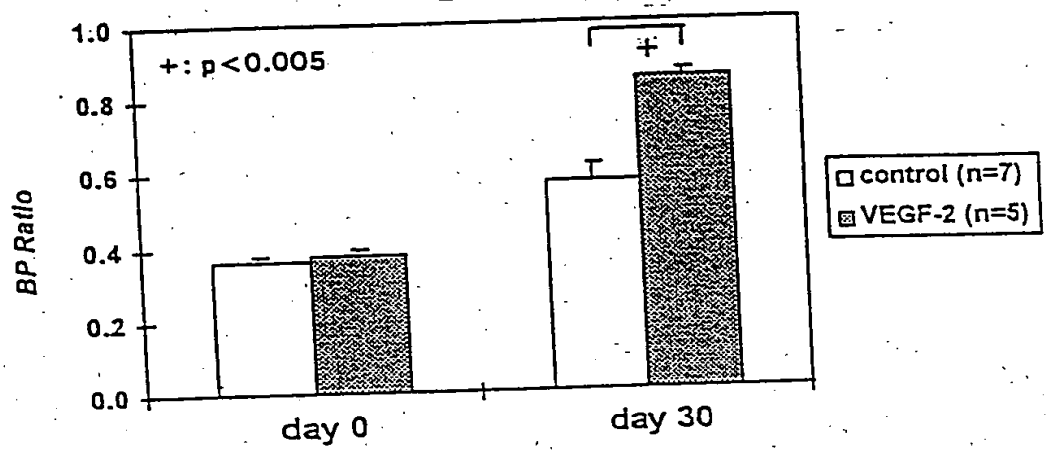


Figure 24

Calf Blood Pressure Ratio
- Protein i.a. -



Calf Blood Pressure Ratio
- Plasmid -



Calf Blood Pressure Ratio

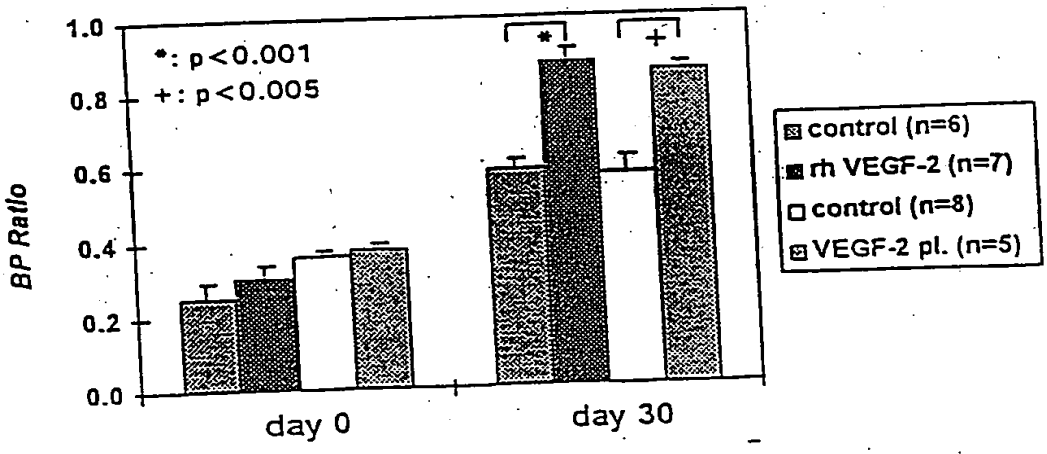


Figure 25A

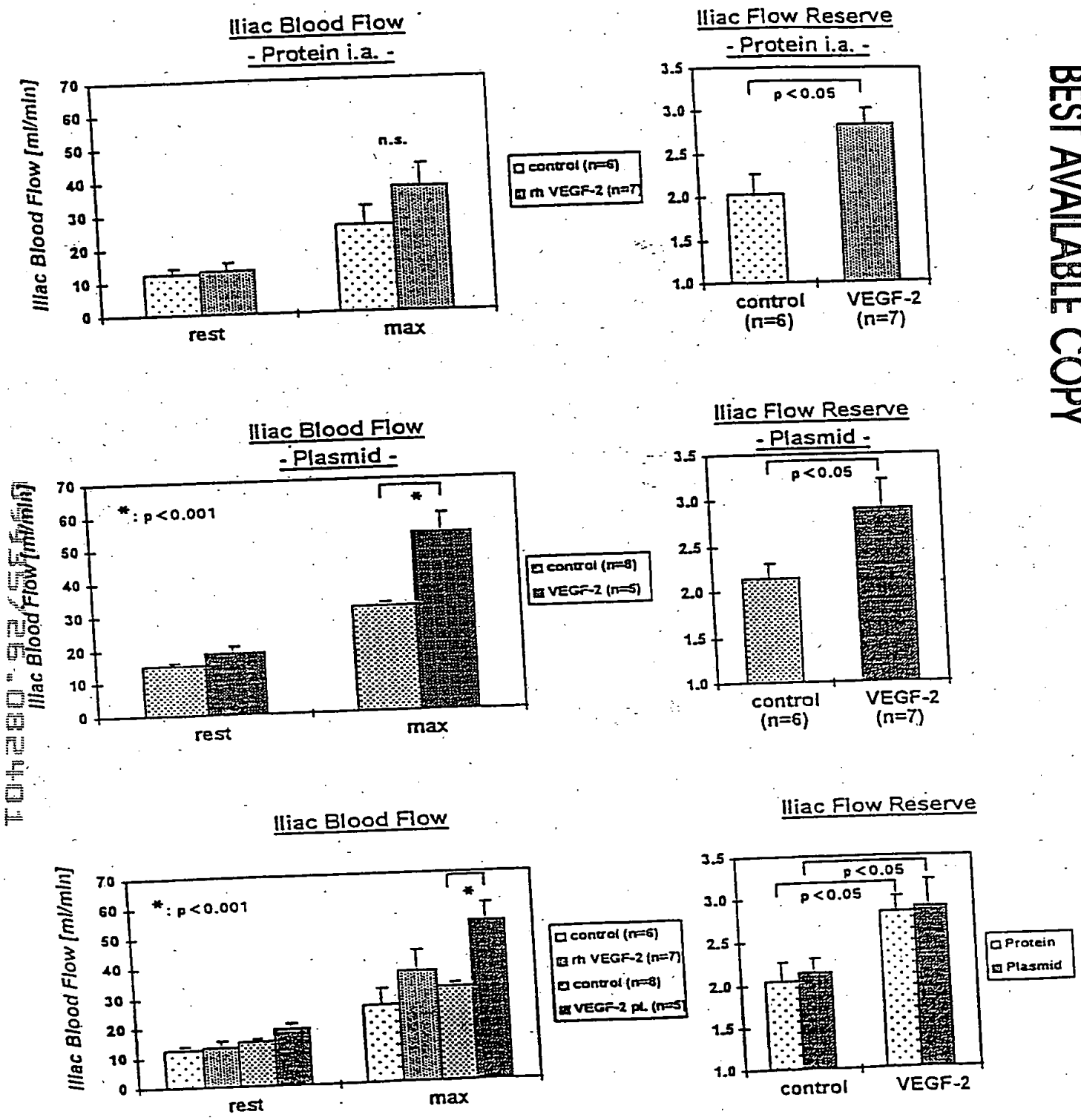


Figure 25B

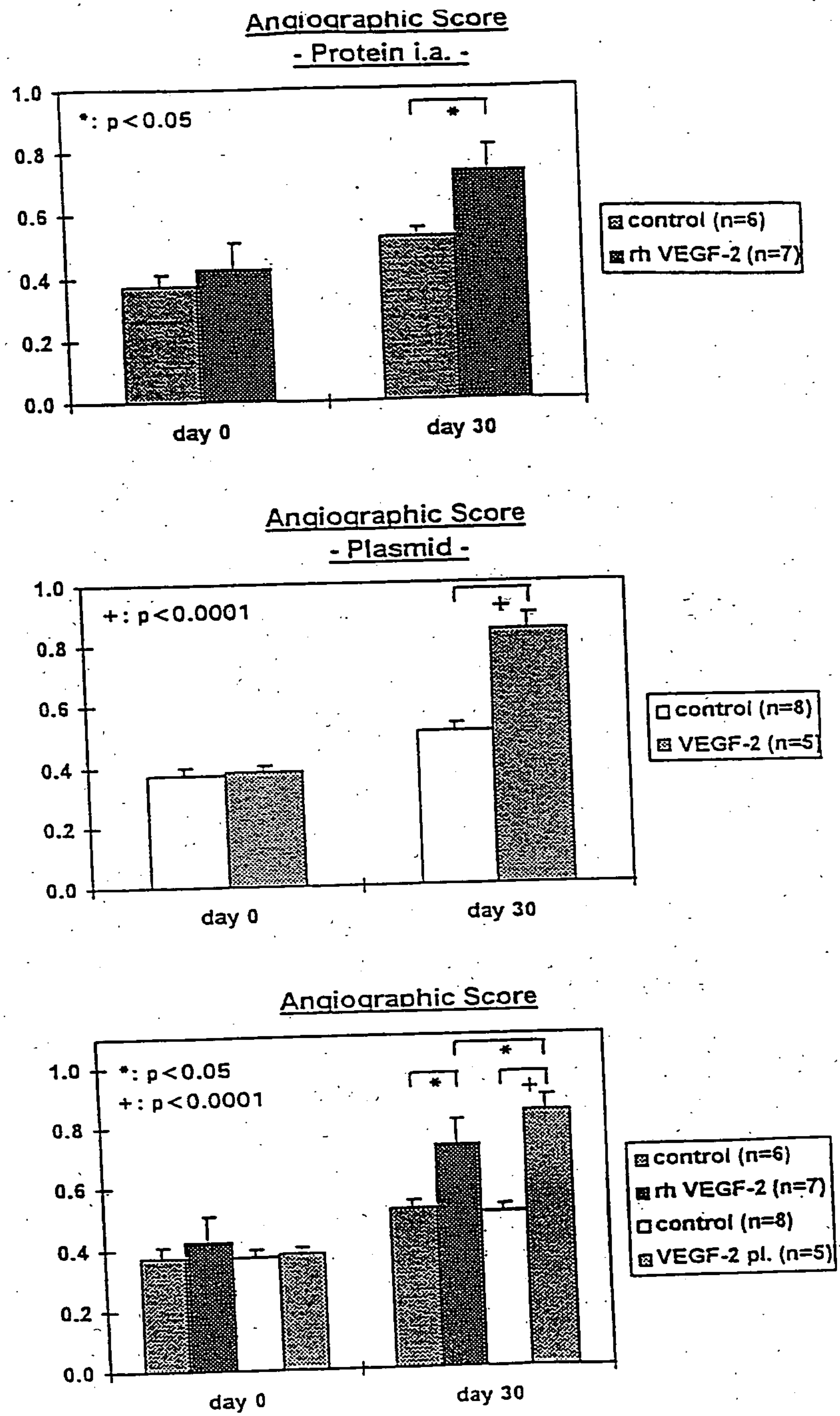

Angiographic Score
- Protein i.a. -
*: p<0.05
control (n=6)
rh VEGF-2 (n=7)
1.0
0.8
0.6
0.4
0.2
0.0
day 0
day 30
Angiographic Score
- Plasmid -
+: p<0.0001
control (n=8)
VEGF-2 (n=5)
1.0
0.8
0.6
0.4
0.2
0.0
day 0
day 30
Angiographic Score
*: p<0.05
+: p<0.0001
control (n=6)
rh VEGF-2 (n=7)
control (n=8)
VEGF-2 pl. (n=5)
1.0
0.8
0.6
0.4
0.2
0.0
day 0
day 30

Figure 25C

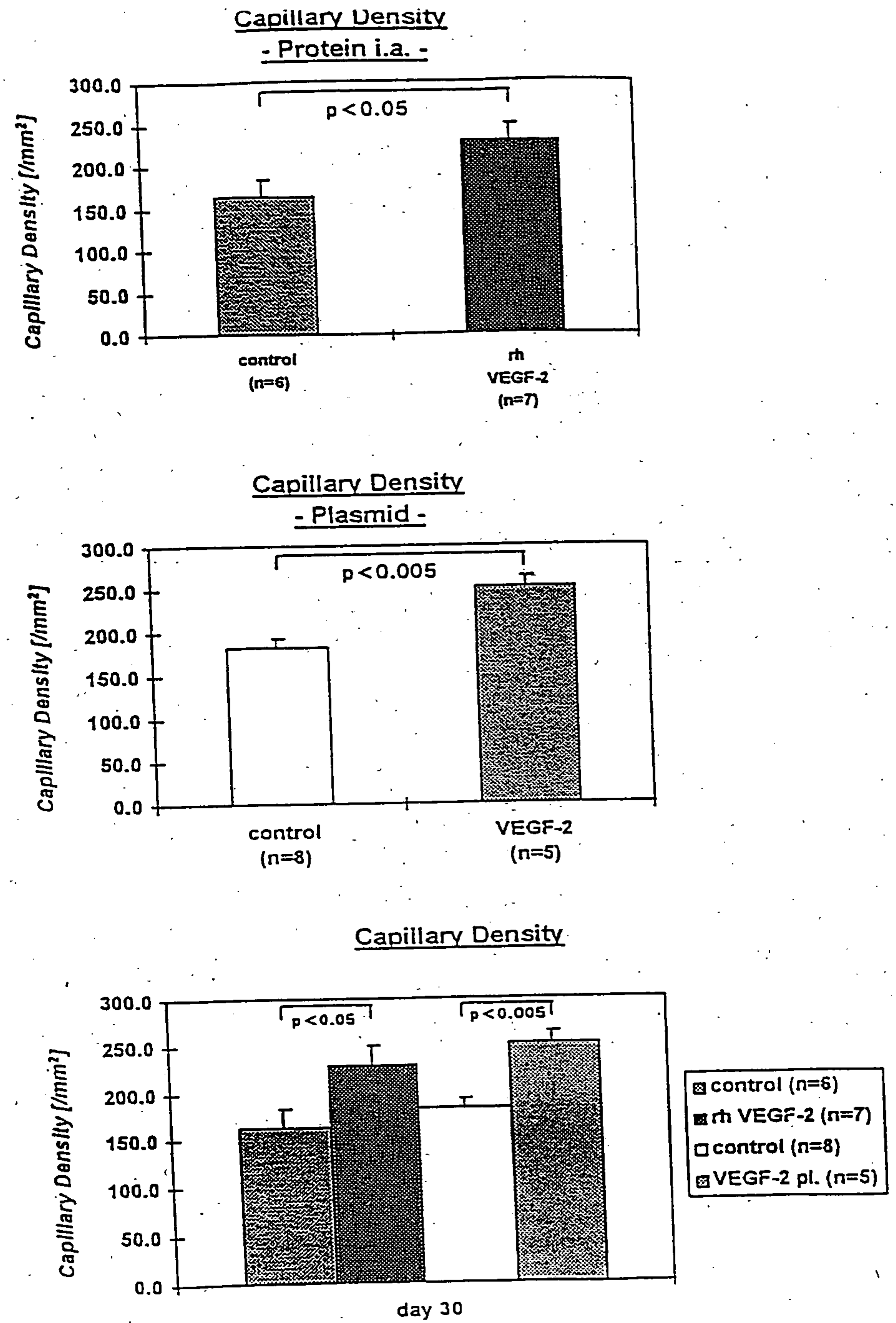

Capillary Density
- Protein i.a. -
300.0
250.0
200.0
150.0
100.0
50.0
0.0
Capillary Density [/mm²]
p < 0.05
control
(n=6)
rh
VEGF-2
(n=7)
Capillary Density
- Plasmid -
300.0
250.0
200.0
150.0
100.0
50.0
0.0
Capillary Density [/mm²]
p < 0.005
control
(n=8)
VEGF-2
(n=5)
Capillary Density
300.0
250.0
200.0
150.0
100.0
50.0
0.0
Capillary Density [/mm²]
p < 0.05
p < 0.005
day 30
control (n=6)
rh VEGF-2 (n=7)
control (n=8)
VEGF-2 pl. (n=5)

Figure 25D

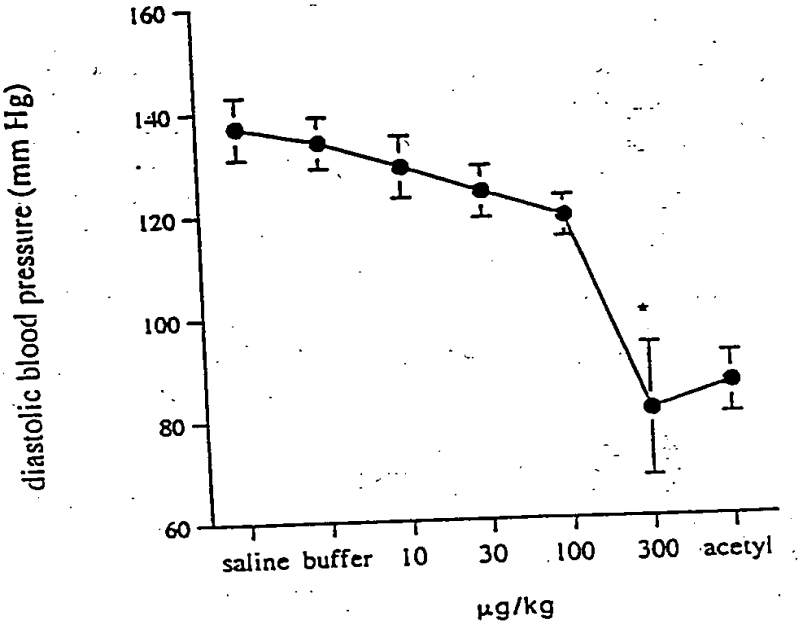


Figure 26A

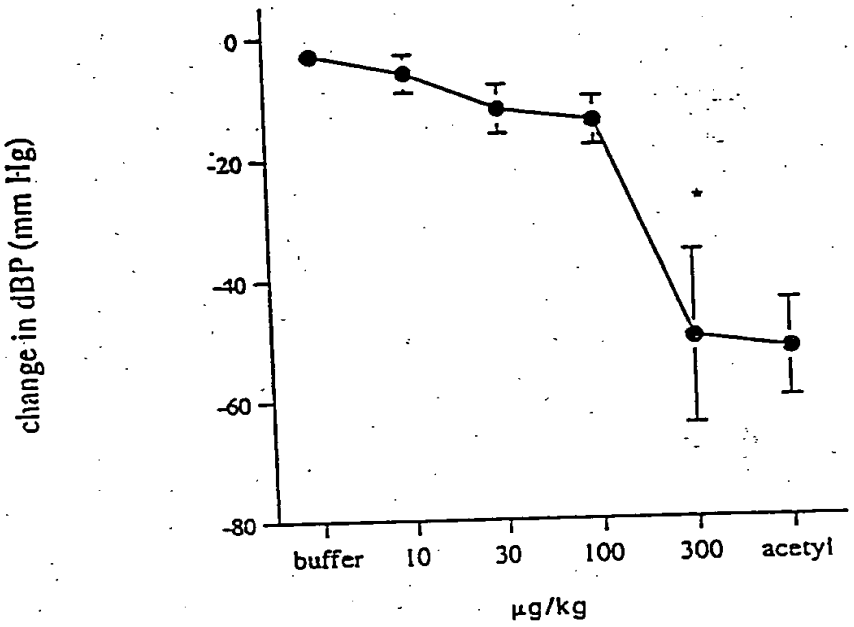


Figure 26B

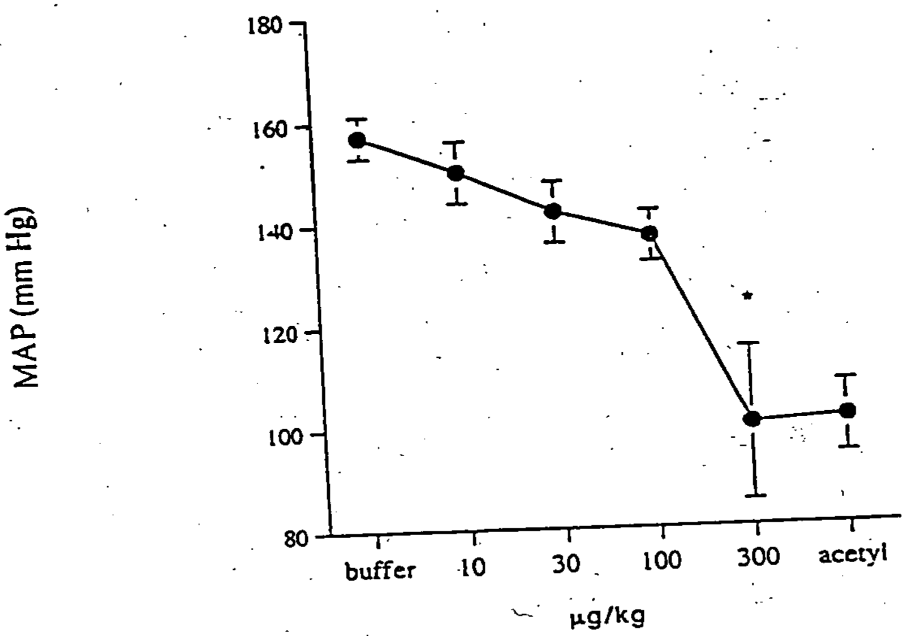

MAP (mm Hg)
180
160
140
120
100
80
*
buffer
10
30
100
300
acetyl
µg/kg

Figure 26C

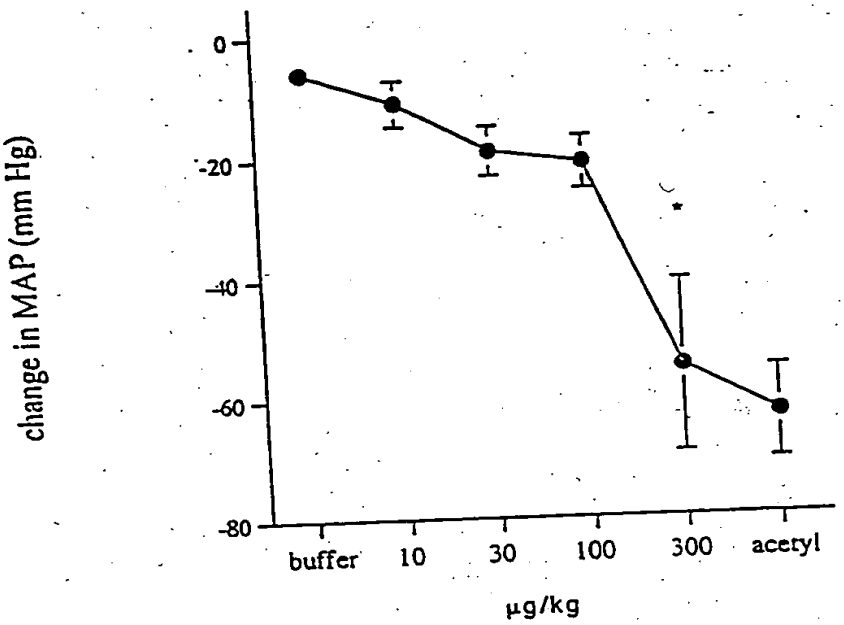
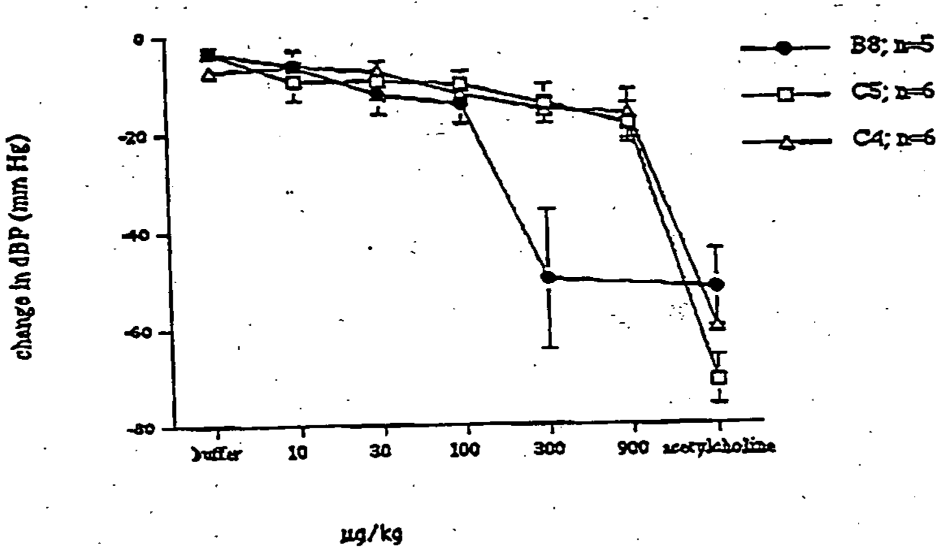


Figure 26D

Change in diastolic blood pressure of SHR rats given increasing doses of VEGF-2

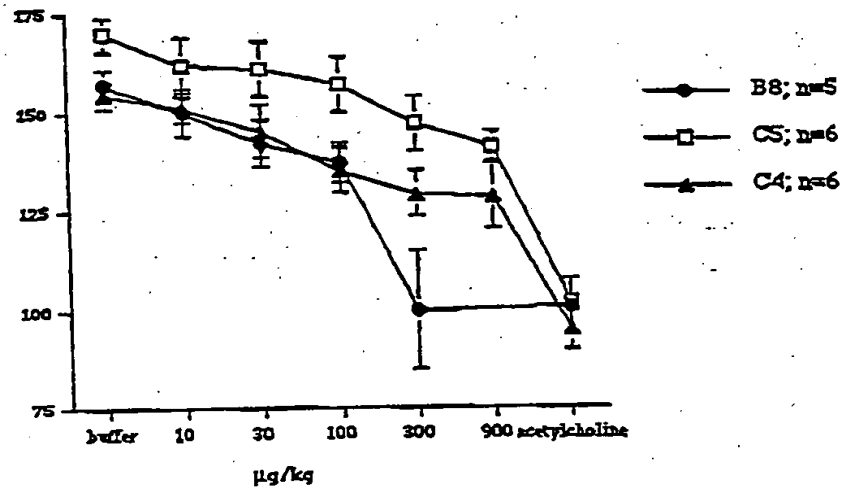


Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, and HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and significance was defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 and C4 were significant at the 300 µg/kg dose. The response to C5 was significant at the 100, 300, and 900 µg/kg doses.

The effect of increasing doses of VEGF-2 on the mean arterial pressure (MAP) of SHR rats

Figure 26E

The effect of increasing doses of VEGF-2 on the mean arterial pressure (MAP) of SHR rats

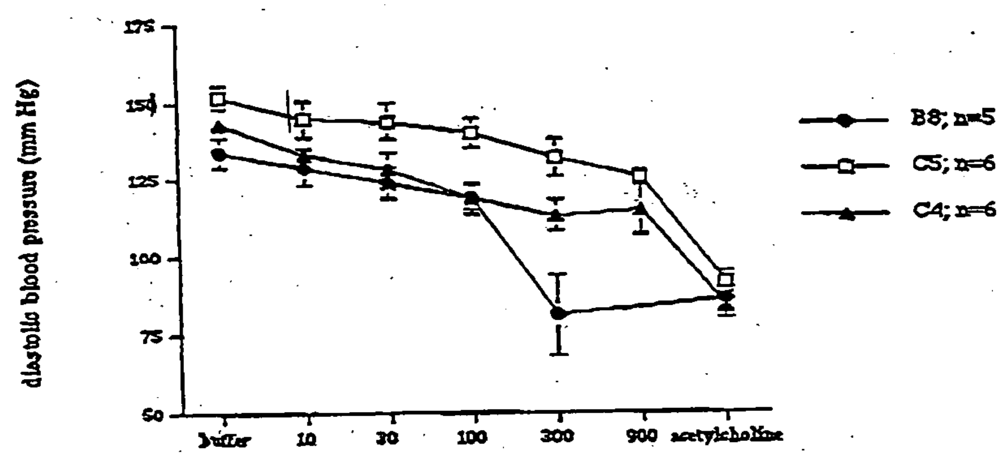


Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, and HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and significance defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 was significant at a 300ng/kg dose. Administration of C5 yielded significant responses at doses greater than or equal to 100 ng/kg. The response to C4 was significant when 10, 100, 300, and 900 ng/kg were given.

The effect of VEGF-2 on the diastolic blood pressure of SHR rats

Figure 26F

The effect of VEGF-2 on the diastolic blood pressure of SHR rats



Increasing doses of VEGF-2 (HG00403-B8, HG00404-C5, HG00404-C4) were administered to 13-14 week old SHR (spontaneously hypertensive rats) and the data are expressed as the mean +/- SEM. Statistical analysis was performed with a paired t-test and statistical significance was defined as $p < 0.05$ vs. the response to buffer alone. The response to B8 was significant only at the 300 µg/kg dose and when given acetylcholine. The responses to C4 and C5, while much less dramatic, were statistically significant at all dose levels.

Figure 26G

VEGF2N.ck

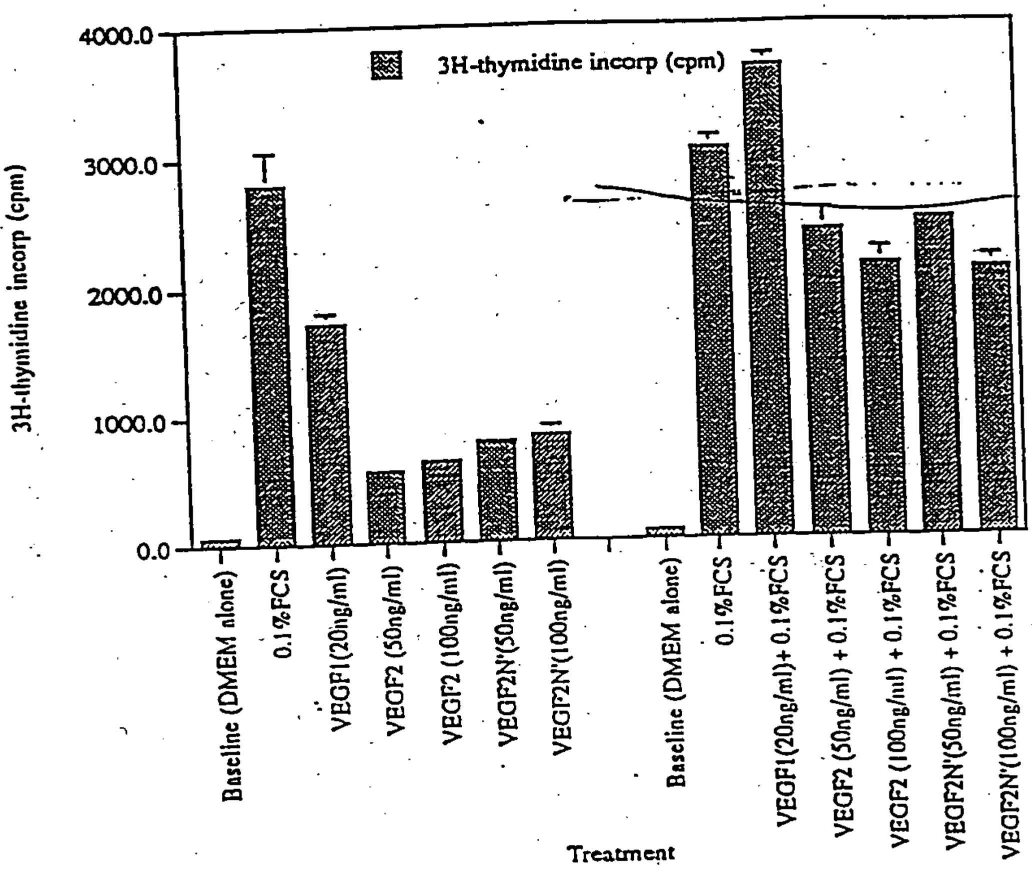


Figure 27

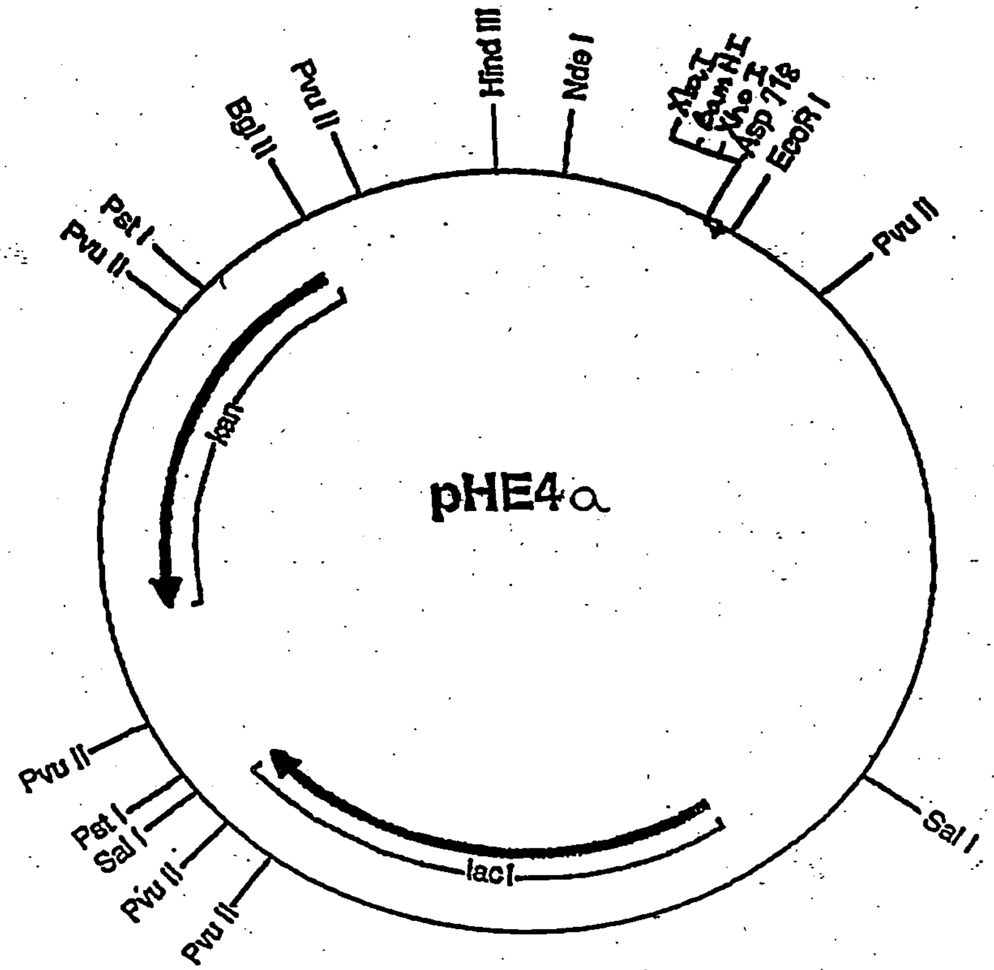

pHE4α
Hind III
Nde I
Xba I
BamHI
Xho I
Asp 718
EcoR I
Pvu II
Sal I
Pvu II
Pvu II
Sal I
Pst I
Pvu II
Pvu II
Pst I
Bgl II
Pvu II
kan
lacI

Figure 28

Figure 29